

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Claims 1-26 (Canceled).

27. (Currently amended) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleotide sequence ~~nucleic acid~~ encoding said polypeptide with at least two primers, wherein said first primer is complementary to a first region of nucleotides of ~~the~~ a nucleic acid of said viral genome, and said second primer is complementary to a second region of nucleotides of ~~the~~ a strand of DNA complementary to said nucleic acid of said viral genome, wherein said first and second regions of nucleotides are separated by about 100 to about 1100 base pairs ~~when said complementary strands are hybridized to form one double-stranded nucleic acid~~, and said at least two primers are selected from the group of nucleotides, oriented in the 5' to 3' direction, consisting of:

SEQ ID NO:68;

nucleotides 6905-6930 (SEQ ID NO:46), 7055-7077 (SEQ ID NO:48), 7360-7384 (SEQ ID NO:49), 7832-7857 (SEQ ID NO:52), 8844-8869 (SEQ ID NO:53), 7629-7647 (SEQ ID NO:55), and 8224-8242 (SEQ ID NO:56) of the *env* gene of HIV-1 Bru;

nucleotides 6930-6905 (SEQ ID NO:47), 7384-7360 (SEQ ID NO:50), 7857-7832 (SEQ ID NO:51), 8869-8844 (SEQ ID NO:54), and nucleotides 8242-8224 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928 (SEQ ID NO:46), 7053-7075 (SEQ ID NO:48), 7349-7373 (SEQ ID NO:49), 7821-7846 (SEQ ID NO:52), 7612-7630 (SEQ ID NO:55), 8213-8231 (SEQ ID NO:56), and 8836-8861 (SEQ ID NO:53) of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903 (SEQ ID NO:47), 7373-7349 (SEQ ID NO:50), 7846-7821 (SEQ ID NO:51), 8861-8836 (SEQ ID NO:54), and 8231-8213 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

nucleotides 6860-6885 (SEQ ID NO:46), 7010-7032 (SEQ ID NO:48), 7306-7330 (SEQ ID NO:49), 7775-7800 (SEQ ID NO:52), 8787-8812 (SEQ ID NO:53), 7572-7590 (SEQ ID NO:55), and 8167-8185 (SEQ ID NO:56) of the *env* gene of HIV-1 Eli; and

nucleotides 6885-6860 (SEQ ID NO:47), 7330-7306 (SEQ ID NO:50), 7800-7775 (SEQ ID NO:51), 8812-8787 (SEQ ID NO:54), and 8185-8167 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli;

- b) introducing said amplified nucleotide sequence into a vector;
- c) transforming a host cell with said vector;
- d) placing said transformed host cell in culture; and
- e) ~~recovering~~ expressing said polypeptide ~~from said culture~~.

28. (Currently amended) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleotide sequence ~~nucleic acid~~ encoding said polypeptide with at least two primers, wherein said first primer is complementary to a first region of nucleotides of the a nucleic acid of said viral genome, and said second primer is complementary to a second region of nucleotides of the a strand of DNA complementary to said nucleic acid of said viral genome, wherein said first and second regions of nucleotides are separated by about 100 to about 1100 base pairs ~~when said complementary strands are hybridized to form one double-stranded nucleic acid~~, and said at least two primers are selected from the group of nucleotides₁ oriented in the 5' to 3' direction₁ consisting of:

MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);
MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);
MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);
MMy7: ATC CTC AGG AGG GGA CCC AGA AAT T (SEQ ID NO:49);
MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);
MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);
MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);
MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);
ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);
MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);
MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);
MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56); and
MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57);

b) introducing said amplified nucleotide sequence into a vector;

- c) transforming a host cell with said vector;
- d) placing said transformed host cell in culture; and
- e) ~~recovering~~ expressing said polypeptide ~~from said culture~~.

Claims 29-31 (Canceled).

32. (Previously presented) A composition comprising at least one polypeptide according to claim 27 in combination with a pharmaceutically acceptable vehicle.

33. (Previously presented) A composition comprising at least one polypeptide according to claim 28 in combination with a pharmaceutically acceptable vehicle.

Claims 34-37 (Canceled).

38. (Currently amended) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

- a) amplifying the nucleotide sequence ~~nucleic acid~~ encoding said polypeptide with at least two primers, wherein said first primer is complementary to a first region of nucleotides of ~~the~~ a nucleic acid of said viral genome, and said second primer is complementary to a second region of nucleotides of ~~the~~ a strand of DNA complementary to said nucleic acid of said viral genome, wherein said first and second regions of nucleotides are separated by about 100 to about 1100 base pairs ~~when said complementary strands are hybridized to form one double-stranded nucleic acid~~, and said at least two primers are selected from the group of nucleotides, oriented in the 5' to 3' direction, consisting of:

SEQ ID NO:68;

nucleotides 6905-6930 (SEQ ID NO:46), 7055-7077 (SEQ ID NO:48), 7360-7384 (SEQ ID NO:49), 7832-7857 (SEQ ID NO:52), 8844-8869 (SEQ ID NO:53), 7629-7647 (SEQ ID NO:55), and 8224-8242 (SEQ ID NO:56) of the *env* gene of HIV-1 Bru;

nucleotides 6930-6905 (SEQ ID NO:47), 7384-7360 (SEQ ID NO:50), 7857-7832 (SEQ ID NO:51), 8869-8844 (SEQ ID NO:54), and nucleotides 8242-8224 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928 (SEQ ID NO:46), 7053-7075 (SEQ ID NO:48), 7349-7373 (SEQ ID NO:49), 7821-7846 (SEQ ID NO:52), 7612-7630 (SEQ ID NO:55), 8213-8231 (SEQ ID NO:56), and 8836-8861 (SEQ ID NO:53) of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903 (SEQ ID NO:47), 7373-7349 (SEQ ID NO:50), 7846-7821 (SEQ ID NO:51), 8861-8836 (SEQ ID NO:54), and 8231-8213 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

nucleotides 6860-6885 (SEQ ID NO:46), 7010-7032 (SEQ ID NO:48), 7306-7330 (SEQ ID NO:49), 7775-7800 (SEQ ID NO:52), 8787-8812 (SEQ ID NO:53), 7572-7590 (SEQ ID NO:55), and 8167-8185 (SEQ ID NO:56) of the *env* gene of HIV-1 Eli;

nucleotides 6885-6860 (SEQ ID NO:47), 7330-7306 (SEQ ID NO:50), 7800-7775 (SEQ ID NO:51), 8812-8787 (SEQ ID NO:54), and 8185-8167 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli; and

a nucleotide sequence that is not identical to anyone of SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, or SEQ ID NO:68, but is nonetheless capable of hybridizing with a nucleotide sequence of the *env* gene of HIV-1 Bru, HIV-1 Mal, and HIV-1 Eli;

- b) introducing said amplified nucleotide sequence into a vector;
- c) transforming a host cell with said vector;
- d) placing said transformed host cell in culture; and
- e) ~~recovering~~ expressing said polypeptide ~~from said culture~~.

39. (Currently amended) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleotide sequence ~~nucleic acid~~ encoding said polypeptide with at least two primers, wherein said first primer is complementary to a first region of nucleotides of ~~the~~ a nucleic acid of said viral genome, and said second primer is complementary to a second region of nucleotides of ~~the~~ a strand of DNA complementary to said nucleic acid of said viral genome, wherein said first and second regions of nucleotides are separated by about 100 to about 1100 base pairs ~~when said complementary strands are hybridized to form one double-stranded nucleic acid~~, and said at least two primers are selected from the group of nucleotides, oriented in the 5' to 3' direction, consisting of:

- MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);
- MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);
- MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);
- MMy7: ATC CTC AGG AGG GGA CCC AGA AAT T (SEQ ID NO:49);
- MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);
- MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);
- MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);

MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);

ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);

MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);

MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);

MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56);

MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57); and

a nucleotide sequence that is not identical to anyone of SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, or SEQ ID NO:68, but is nonetheless capable of hybridizing with a nucleotide sequence of the *env* gene of HIV-1 Bru, HIV-1 Mal, and HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) ~~recovering~~ expressing said polypeptide ~~from said culture~~.

Claims 40-42 (Canceled).

43. (Previously presented) A composition comprising at least one polypeptide according to claim 38 in combination with a pharmaceutically acceptable vehicle.

44. (Previously presented) A composition comprising at least one polypeptide according to claim 39 in combination with a pharmaceutically acceptable vehicle.

Claims 45-48 (Canceled).

49. (Previously presented) The polypeptide according to claim 27, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

50. (Previously presented) The polypeptide according to claim 28, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

51. (Previously presented) The polypeptide according to claim 38, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

52. (Previously presented) The polypeptide according to claim 39, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

53. (Previously presented) The polypeptide according to claim 49, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

54. (Previously presented) The polypeptide according to claim 50, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

55. (Previously presented) The polypeptide according to claim 51, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

56. (Previously presented) The polypeptide according to claim 52, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

57. (Previously presented) The composition according to claim 32, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

58. (Previously presented) The composition according to claim 33, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

59. (Previously presented) The composition according to claim 43, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

60. (Previously presented) The composition according to claim 44, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

61. (Previously presented) The composition according to claim 57, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

62. (Previously presented) The composition according to claim 58, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

63. (Previously presented) The composition according to claim 59, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

64. (Previously presented) The composition according to claim 60, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

65. (New) The polypeptide according to claim 27, wherein the viral genome is HIV-1.

66. (New) The polypeptide according to claim 28, wherein the viral genome is HIV-1.

67. (New) The polypeptide according to claim 38, wherein the viral genome is HIV-1.

68. (New) The polypeptide according to claim 39, wherein the viral genome is HIV-1.